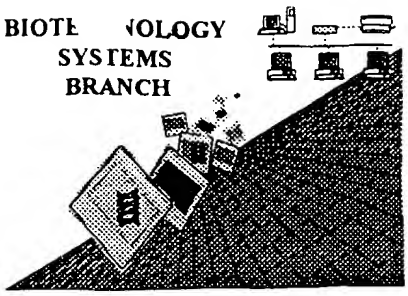

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/763,777

Source: PCT09

Date Processed by STIC: 3/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

PCT09

RAW SEQUENCE LISTING DATE: 03/07/2001
PATENT APPLICATION: US/09/763,777 TIME: 13:12:46

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03072001\I763777.raw

Does Not Comply
Corrected Diskette Needed
pr 1-2

<110> APPLICANT: Thakur, Madhukar L.
<120> TITLE OF INVENTION: Imaging With TC-99M Labeled Fibrin-Alpha-Chain Peptide
<130> FILE REFERENCE: THA01-NP003
C> <140> CURRENT APPLICATION NUMBER: US/09/763,777
C-> <141> CURRENT FILING DATE: 2001-02-16
<150> PRIOR APPLICATION NUMBER: 60/096,803
<151> PRIOR FILING DATE: 1998-08-17
<160> NUMBER OF SEQ ID NOS: 5
<170> SOFTWARE: FastSEQ for Windows Version 4.0
<210> SEQ ID NO: 1
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: N-terminus tripeptide portion of fibrin alpha-chain polypeptide
<400> SEQUENCE: 1
Gly Pro Arg
1
<210> SEQ ID NO: 2
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Analog of N-terminus tripeptide identified in SEQ ID:1
<400> SEQUENCE: 2
Gly Pro Arg Pro
1
<210> SEQ ID NO: 3
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: pentapeptide analog related to N-terminus portion of fibrin alpha chain polypeptide
<400> SEQUENCE: 3
Gly Pro Arg Pro Pro
1 5
<210> SEQ ID NO: 4
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: at amino acid number 2 the Alanine is the D-alanine

see item 12 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 03/07/2001
PATENT APPLICATION: US/09/763,777 TIME: 13:12:46

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03072001\I763777.raw

```
69 <400> SEQUENCE: 4
70 Gly Ala Gly Gly
71  1
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 10
75 <212> TYPE: PRT
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:                                          <2217
79 <223> OTHER INFORMATION: TP 850 decapeptide             <2227
81 <223> OTHER INFORMATION: at amino acid number 6 Xaa designates Aba which is
82       4-aminobutyric acid
84 <223> OTHER INFORMATION: at amino acid number 9 the Alanine is the
85       D-alanine
87 <400> SEQUENCE: 5
88 Gly Pro Arg Pro Pro Xaa Gly Gly Ala Gly
89  1               5                  10
```

see 1.823 of new Sequence Rules for explanation.

These two numeric identifiers are mandatory when n's or Xaa's are shown.

VERIFICATION SUMMARY DATE: 03/07/2001
PATENT APPLICATION: US/09/763,777 TIME: 13:12:47

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\03072001\I763777.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:88 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:88 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:88 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/763,777

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.